Elizabeth S Dennis

List of Publications by Year
in descending order

306 papers	33,976 citations	2215 99 h-index	4342 173 g-index
311 all docs	311 docs citations	311 times ranked	18207 citing authors

#	Article	IF	Citations
1	Sequencing of allotetraploid cotton (Gossypium hirsutum L. acc. TM-1) provides a resource for fiber improvement. Nature Biotechnology, 2015, 33, 531-537.	17.5	1,560
2	Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibres. Nature, 2012, 492, 423-427.	27.8	1,204
3	The FLF MADS Box Gene: A Repressor of Flowering in Arabidopsis Regulated by Vernalization and Methylation. Plant Cell, 1999, 11, 445-458.	6.6	905
4	Reduced DNA methylation in Arabidopsis thaliana results in abnormal plant development.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 8449-8454.	7.1	703
5	The Arabidopsis FLC protein interacts directlyin vivowithSOC1andFTchromatin and is part of a high-molecular-weight protein complex. Plant Journal, 2006, 46, 183-192.	5.7	502
6	Fertilization-independent seed development in <i>Arabidopsisâ€‰thaliana</i>. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 4223-4228.	7.1	487
7	MINISEED3 (MINI3), a WRKY family gene, and HAIKU2 (IKU2), a leucine-rich repeat (LRR) KINASE gene, are regulators of seed size in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17531-17536.	7.1	476
8	Genes controlling fertilization-independent seed development in <i>Arabidopsis thaliana</i>. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 296-301.	7.1	436
9	Expression and parent-of-origin effects for <i>FIS2</i> , <i>MEA</i> , and <i>FIE</i> in the endosperm and embryo of developing <i>Arabidopsis</i> seeds. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 10637-10642.	7.1	413
10	MADS box genes control vernalization-induced flowering in cereals. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13099-13104.	7.1	409
11	Toward Sequencing Cotton (<i>Gossypium</i>) Genomes: Figure 1.. Plant Physiology, 2007, 145, 1303-1310.	4.8	390
12	HKT1;5-Like Cation Transporters Linked to Na+ Exclusion Loci in Wheat, Nax2 and Kna1. Plant Physiology, 2007, 143, 1918-1928.	4.8	378
13	The molecular basis of vernalization: The central role of FLOWERING LOCUS C (FLC). Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 3753-3758.	7.1	366
14	Expression Profile Analysis of the Low-Oxygen Response in Arabidopsis Root Cultures[W]. Plant Cell, 2002, 14, 2481-2494.	6.6	362
15	Molecular analysis of the alcohol dehydrogenase (Adhl) gene of maize. Nucleic Acids Research, 1984, 12, 3983-4000.	14.5	353
16	The molecular basis of vernalization-induced flowering in cereals. Trends in Plant Science, 2007, 12, 352-357.	8.8	340
17	Chitinase, beta-1,3-glucanase, osmotin, and extensin are expressed in tobacco explants during flower formation.. Plant Cell, 1990, 2, 673-684.	6.6	338
18	The Arabidopsis thaliana vernalization response requires a polycomb-like protein complex that also includes VERNALIZATION INSENSITIVE 3. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14631-14636.	7.1	335

#	Article	IF	Citations
19	Nomenclature for HKT transporters, key determinants of plant salinity tolerance. Trends in Plant Science, 2006, 11, 372-374.	8.8	329
20	FLOWERING LOCUS C (FLC) regulates development pathways throughout the life cycle of <i>Arabidopsis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6680-6685.	7.1	325
21	amp1 - a mutant with high cytokinin levels and altered embryonic pattern, faster vegetative growth, constitutive photomorphogenesis and precocious flowering. Plant Journal, 1993, 4, 907-916.	5.7	316
22	Molecular and chromosomal organization of DNA sequences coding for the ribosomal RNAs in cereals. Chromosoma, 1980, 78, 293-311.	2.2	315
23	Changes in 24-nt siRNA levels in Arabidopsis hybrids suggest an epigenetic contribution to hybrid vigor. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2617-2622.	7.1	310
24	Cold-induced repression of the rice anther-specific cell wall invertase gene OSINV4 is correlated with sucrose accumulation and pollen sterility. Plant, Cell and Environment, 2005, 28, 1534-1551.	5.7	309
25	Highly repeated DNA sequence limited to knob heterochromatin in maize. Proceedings of the National Academy of Sciences of the United States of America, 1981, 78, 4490-4494.	7.1	302
26	DNA methylation, vernalization, and the initiation of flowering.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 287-291.	7.1	301
27	The MYB transcription factor GhMYB25 regulates early fibre and trichome development. Plant Journal, 2009, 59, 52-62.	5.7	297
28	Arabidopsis<i>RAP2.2</i>: An Ethylene Response Transcription Factor That Is Important for Hypoxia Survival Â Â. Plant Physiology, 2010, 153, 757-772.	4.8	293
29	<i>GAMYB-like</i> Genes, Flowering, and Gibberellin Signaling in Arabidopsis. Plant Physiology, 2001, 127, 1682-1693.	4.8	291
30	Differential Interactions of Promoter Elements in Stress Responses of the Arabidopsis Adh Gene. Plant Physiology, 1994, 105, 1075-1087.	4.8	286
31	On the role of RNA silencing in the pathogenicity and evolution of viroids and viral satellites. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 3275-3280.	7.1	273
32	The transcription factor ATAF2 represses the expression of pathogenesis-related genes in Arabidopsis. Plant Journal, 2005, 43, 745-757.	5.7	273
33	ABA Regulates Apoplastic Sugar Transport and is a Potential Signal for Cold-Induced Pollen Sterility in Rice. Plant and Cell Physiology, 2007, 48, 1319-1330.	3.1	271
34	A Sodium Transporter (HKT7) Is a Candidate for Nax1, a Gene for Salt Tolerance in Durum Wheat. Plant Physiology, 2006, 142, 1718-1727.	4.8	266
35	Molecular analysis of the alcohol dehydrogenase 2 (Adh2) gene of maize. Nucleic Acids Research, 1985, 13, 727-743.	14.5	262
36	Isolation and identification by sequence homology of a putative cytosine methyltransferase fromArabidopsis thaliana. Nucleic Acids Research, 1993, 21, 2383-2388.	14.5	258

#	Article	IF	Citations
37	Two hemoglobin genes in Arabidopsis thaliana: The evolutionary origins of leghemoglobins. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 12230-12234.	7.1	253
38	The molecular biology of seasonal flowering-responses in Arabidopsis and the cereals. Annals of Botany, 2009, 103, 1165-1172.	2.9	245
39	Different Regulatory Regions Are Required for the Vernalization-Induced Repression of FLOWERING LOCUS C and for the Epigenetic Maintenance of Repression. Plant Cell, 2002, 14, 2527-2537.	6.6	243
40	Enhanced Low Oxygen Survival in Arabidopsis through Increased Metabolic Flux in the Fermentative Pathway. Plant Physiology, 2003, 132, 1292-1302.	4.8	243
41	DNA demethylases target promoter transposable elements to positively regulate stress responsive genes in Arabidopsis. Genome Biology, 2014, 15, 458.	8.8	243
42	DNA methylation, a key regulator of plant development and other processes. Current Opinion in Genetics and Development, 2000, 10, 217-223.	3.3	240
43	GhMYB25â€like: a key factor in early cotton fibre development. Plant Journal, 2011, 65, 785-797.	5.7	229
44	The VQ motif protein IKU1 regulates endosperm growth and seed size in Arabidopsis. Plant Journal, 2010, 63, 670-679.	5.7	224
45	DNA sequences required for anaerobic expression of the maize alcohol dehydrogenase 1 gene. Proceedings of the National Academy of Sciences of the United States of America, 1987, 84, 6624-6628.	7.1	221
46	Vernalization-Induced Trimethylation of Histone H3 Lysine 27 at FLC Is Not Maintained in Mitotically Quiescent Cells. Current Biology, 2007, 17, 1978-1983.	3.9	221
47	Low-Temperature and Daylength Cues Are Integrated to Regulate <i>FLOWERING LOCUS T</i> in Barley Â Â Â. Plant Physiology, 2008, 147, 355-366.	4.8	212
48	HvVRN2 Responds to Daylength, whereas HvVRN1 Is Regulated by Vernalization and Developmental Status. Plant Physiology, 2006, 140, 1397-1405.	4.8	209
49	Vernalization-induced flowering in cereals is associated with changes in histone methylation at the <i>VERNALIZATION1</i> gene. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 8386-8391.	7.1	208
50	Cloning of the Arabidopsis ent-kaurene oxidase gene GA3. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 9019-9024.	7.1	205
51	DNA methylation and the promotion of flowering by vernalization. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 5824-5829.	7.1	205
52	Mitochondrial DNA sequences in ancient Australians: Implications for modern human origins. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 537-542.	7.1	204
53	Trans Chromosomal Methylation in <i>Arabidopsis</i> hybrids. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3570-3575.	7.1	202
54	Functioning haemoglobin genes in non-nodulating plants. Nature, 1988, 331, 178-180.	27.8	200

#	Article	IF	Citations
55	Control of flowering time by FLC orthologues in Brassica napus. Plant Journal, 2001, 28, 545-553.	5.7	197
56	Expression, Imprinting, and Evolution of Rice Homologs of the Polycomb Group Genes. Molecular Plant, 2009, 2, 711-723.	8.3	193
57	Arabidopsis Roots and Shoots Have Different Mechanisms for Hypoxic Stress Tolerance. Plant Physiology, 1999, 119, 57-64.	4.8	190
58	pEmu: an improved promoter for gene expression in cereal cells. Theoretical and Applied Genetics, 1991, 81, 581-588.	3.6	188
59	Resetting of <i>FLOWERING LOCUS C</i> expression after epigenetic repression by vernalization. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2214-2219.	7.1	187
60	Evidence for a Role for AtMYB2 in the Induction of the Arabidopsis Alcohol Dehydrogenase Gene (ADH1) by Low Oxygen. Genetics, 1998, 149, 479-490.	2.9	186
61	Abscisic Acid Induces the Alcohol Dehydrogenase Gene in Arabidopsis. Plant Physiology, 1996, 111, 381-391.	4.8	184
62	Control of Early Seed Development. Annual Review of Cell and Developmental Biology, 2001, 17, 677-699.	9.4	184
63	Hypoxia-responsive microRNAs and trans-acting small interfering RNAs in Arabidopsis. Journal of Experimental Botany, 2010, 61, 165-177.	4.8	184
64	Arabidopsis ent-Kaurene Oxidase Catalyzes Three Steps of Gibberellin Biosynthesis. Plant Physiology, 1999, 119, 507-510.	4.8	182
65	A hemoglobin from plants homologous to truncated hemoglobins of microorganisms. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 10119-10124.	7.1	182
66	Global Gene Expression Responses to Waterlogging in Roots and Leaves of Cotton (Gossypium) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3	3.1	177
67	Transposase activity of the Ac controlling element in maize is regulated by its degree of methylation. Molecular Genetics and Genomics, 1986, 205, 476-482.	2.4	175
68	Short Vegetative Phase-Like MADS-Box Genes Inhibit Floral Meristem Identity in Barley. Plant Physiology, 2007, 143, 225-235.	4.8	174
69	Epigenetic regulation of flowering. Current Opinion in Plant Biology, 2007, 10, 520-527.	7.1	172
70	Increased level of hemoglobin 1 enhances survival of hypoxic stress and promotes early growth in Arabidopsis thaliana. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 17197-17202.	7.1	170
71	Expression Profiling Identifies Genes Expressed Early During Lint Fibre Initiation in Cotton. Plant and Cell Physiology, 2006, 47, 107-127.	3.1	165
72	The CYP88A cytochrome P450, ent-kaurenoic acid oxidase, catalyzes three steps of the gibberellin biosynthesis pathway. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 2065-2070.	7.1	164

#	Article	IF	Citations
73	Heterosis of <i>Arabidopsis</i> hybrids between C24 and Col is associated with increased photosynthesis capacity. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7109-7114.	7.1	161
74	A new hemoglobin gene from soybean: a role for hemoglobin in all plants.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 5682-5687.	7.1	152
75	The ANTHER INDEHISCENCE1 Gene Encoding a Single MYB Domain Protein Is Involved in Anther Development in Rice. Plant Physiology, 2004, 135, 1514-1525.	4.8	152
76	The Arabidopsis <i>AMP1</i> Gene Encodes a Putative Glutamate Carboxypeptidase. Plant Cell, 2001, 13, 2115-2125.	6.6	146
77	cDNA cloning and induction of the alcohol dehydrogenase gene (Adh1) of maize. Proceedings of the National Academy of Sciences of the United States of America, 1982, 79, 2981-2985.	7.1	145
78	A plastid envelope location of Arabidopsis ent-kaurene oxidase links the plastid and endoplasmic reticulum steps of the gibberellin biosynthesis pathway. Plant Journal, 2001, 28, 201-208.	5.7	143
79	The Low-Oxygen-Induced NAC Domain Transcription Factor <i>ANAC102</i> Affects Viability of Arabidopsis Seeds following Low-Oxygen Treatment Â Â. Plant Physiology, 2009, 149, 1724-1738.	4.8	141
80	Expression and evolution of functionally distinct haemoglobin genes in plants. Plant Molecular Biology, 2001, 47, 677-692.	3.9	139
81	A global assembly of cotton ESTs. Genome Research, 2006, 16, 441-450.	5.5	138
82	The role of epigenetics in hybrid vigour. Trends in Genetics, 2013, 29, 684-690.	6.7	137
83	OCSBF-1, a maize ocs enhancer binding factor: isolation and expression during development.. Plant Cell, 1990, 2, 891-903.	6.6	136
84	The control of flowering by vernalization. Current Opinion in Plant Biology, 2000, 3, 418-422.	7.1	126
85	The downregulation of FLOWERING LOCUS C (FLC) expression in plants with low levels of DNA methylation and by vernalization occurs by distinct mechanisms. Plant Journal, 2005, 44, 420-432.	5.7	125
86	Epidermal cell differentiation in cotton mediated by the homeodomain leucine zipper gene, <i>GhHDâ€1</i>. Plant Journal, 2012, 71, 464-478.	5.7	125
87	Common evolutionary origin of legume and non-legume plant haemoglobins. Nature, 1986, 324, 166-168.	27.8	124
88	Cloning and characterization of<i>MS5</i>from<i>Arabidopsis</i>: a gene critical in male meiosis. Plant Journal, 1998, 15, 345-356.	5.7	121
89	Vernalization-Repression of Arabidopsis FLC Requires Promoter Sequences but Not Antisense Transcripts. PLoS ONE, 2011, 6, e21513.	2.5	121
90	Identical polypyrimidine-polypurine satellite DNAs in wheat and barley. Heredity, 1980, 44, 349-366.	2.6	120

#	Article	IF	Citations
91	Two repeated DNA sequences from the heterochromatic regions of rye (Secale cereale) chromosomes. Chromosoma, 1981, 84, 265-277.	2.2	120
92	Spatial and temporal analysis of the local response to wounding. Plant Molecular Biology, 2004, 55, 165-181.	3.9	120
93	Review: Correlations between oxygen affinity and sequence classifications of plant hemoglobins. Biopolymers, 2009, 91, 1083-1096.	2.4	120
94	Transcript Profiling During Fiber Development Identifies Pathways in Secondary Metabolism and Cell Wall Structure That May Contribute to Cotton Fiber Quality. Plant and Cell Physiology, 2009, 50, 1364-1381.	3.1	120
95	Characterization of the defense transcriptome responsive to Fusarium oxysporum-infection in Arabidopsis using RNA-seq. Gene, 2013, 512, 259-266.	2.2	120
96	FLC, a repressor of flowering, is regulated by genes in different inductive pathways. Plant Journal, 2002, 29, 183-191.	5.7	116
97	Hormone-regulated defense and stress response networks contribute to heterosis in<i>Arabidopsis</i>F1 hybrids. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6397-406.	7.1	110
98	Recent research on the mechanism of heterosis is important for crop and vegetable breeding systems. Breeding Science, 2018, 68, 145-158.	1.9	110
99	Isolation and molecular analysis of the maize P locus. Molecular Genetics and Genomics, 1989, 219, 225-234.	2.4	109
100	The influence of vernalization and daylength on expression of flowering-time genes in the shoot apex and leaves of barley (Hordeum vulgare).. Journal of Experimental Botany, 2009, 60, 2169-2178.	4.8	107
101	A role for haemoglobin in all plant roots?. Plant, Cell and Environment, 1988, 11, 359-367.	5.7	105
102	Genetic and physical mapping of flowering time loci in canola (Brassica napus L.). Theoretical and Applied Genetics, 2013, 126, 119-132.	3.6	105
103	Regions associated with repression of the barley (Hordeum vulgare) VERNALIZATION1 gene are not required for cold induction. Molecular Genetics and Genomics, 2009, 282, 107-117.	2.1	103
104	Knob heterochromatin homology in maize and its relatives. Journal of Molecular Evolution, 1984, 20, 341-350.	1.8	102
105	Epigenetic Changes in Hybrids. Plant Physiology, 2015, 168, 1197-1205.	4.8	102
106	Eucalyptus has a functional equivalent of the Arabidopsis floral meristem identity gene LEAFY. Plant Molecular Biology, 1998, 37, 897-910.	3.9	100
107	Molecular analysis of a somaclonal mutant of maize alcohol dehydrogenase. Molecular Genetics and Genomics, 1986, 202, 235-239.	2.4	98
108	Quantitative effects of vernalization onFLCandSOC1expression. Plant Journal, 2006, 45, 871-883.	5.7	98

#	Article	IF	Citations
109	The Arabidopsis AMP1 Gene Encodes a Putative Glutamate Carboxypeptidase. Plant Cell, 2001, 13, 2115-2125.	6.6	98
110	Arabidopsis Polycomb Repressive Complex 2 binding sites contain putative GAGA factor binding motifs within coding regions of genes. BMC Genomics, 2013, 14, 593.	2.8	94
111	Structure and expression of an alcohol dehydrogenase 1 gene from Pisum sativum (cv. â€œGreenfeastâ€). Journal of Molecular Biology, 1987, 195, 115-123.	4.2	93
112	Title is missing!. Molecular Breeding, 1997, 3, 371-380.	2.1	93
113	Functional properties of the anaerobic responsive element of the maize Adh1 gene. Plant Molecular Biology, 1990, 15, 593-604.	3.9	91
114	Enhancement of Submergence Tolerance in Transgenic Rice Overproducing Pyruvate Decarboxylase. Journal of Plant Physiology, 2000, 156, 516-521.	3.5	90
115	Increased endogenous cytokinin in the Arabidopsis amp1 mutant corresponds with de-etiolation responses. Planta, 1996, 198, 549-556.	3.2	89
116	<i>ODDSOC2</i> Is a MADS Box Floral Repressor That Is Down-Regulated by Vernalization in Temperate Cereals Â Â. Plant Physiology, 2010, 153, 1062-1073.	4.8	88
117	Eucalyptus has functional equivalents of the Arabidopsis AP1 gene. Plant Molecular Biology, 1997, 35, 573-584.	3.9	87
118	Regeneration and transformation of Eucalyptus camaldulensis. Plant Cell Reports, 1997, 16, 787-791.	5.6	85
119	The anaerobic responsive element contains two GC-rich sequences essential for binding a nuclear protien and hypoxic activation of the maizeAdh1promoter. Nucleic Acids Research, 1991, 19, 7053-7060.	14.5	84
120	Regulated expression of an alcohol dehydrogenase 1 chimeric gene introduced into maize protoplasts. Planta, 1987, 170, 535-540.	3.2	83
121	Genes conferring late flowering inArabidopsis thaliana. Genetica, 1993, 90, 147-155.	1.1	83
122	The Cytotoxic Plant Protein, Î²-Purothionin, Forms Ion Channels in Lipid Membranes. Journal of Biological Chemistry, 2000, 275, 823-827.	3.4	83
123	Reciprocal control of flowering time by OsSOC1 in transgenic Arabidopsis and by FLC in transgenic rice. Plant Biotechnology Journal, 2003, 1, 361-369.	8.3	81
124	Highly repeated DNA in Drosophila melanogaster. Journal of Molecular Biology, 1977, 112, 31-47.	4.2	80
125	ATAF NAC transcription factors: Regulators of plant stress signaling. Plant Signaling and Behavior, 2010, 5, 428-432.	2.4	80
126	Reactivation of a silent Ac following tissue culture is associated with heritable alterations in its methylation pattern. Molecular Genetics and Genomics, 1991, 229, 365-372.	2.4	78

#	Article	IF	Citations
127	Intraspecific Arabidopsis Hybrids Show Different Patterns of Heterosis Despite the Close Relatedness of the Parental Genomes Â Â. Plant Physiology, 2014, 166, 265-280.	4.8	77
128	Genetic control of male fertility in Arabidopsis thaliana : structural analyses of postmeiotic developmental mutants. Planta, 1998, 205, 492-505.	3.2	75
129	Hemoglobin is essential for normal growth of Arabidopsis organs. Physiologia Plantarum, 2006, 127, 157-166.	5.2	75
130	A Cluster of Arabidopsis Genes with a Coordinate Response to an Environmental Stimulus. Current Biology, 2004, 14, 911-916.	3.9	74
131	Does the ocs-element occur as a functional component of the promoters of plant genes?. Plant Journal, 1993, 4, 433-443.	5.7	72
132	Role of DNA methylation in hybrid vigor in <i>Arabidopsis thaliana</i>. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6704-E6711.	7.1	71
133	Multiple DNA methyltransferase genes in Arabidopsis thaliana. Plant Molecular Biology, 1999, 41, 269-278.	3.9	70
134	Insect- and herbicide-resistant transgenic eucalypts*. Molecular Breeding, 2000, 6, 307-315.	2.1	70
135	Laser capture microdissection and cDNA microarrays used to generate gene expression profiles of the rapidly expanding fibre initial cells on the surface of cotton ovules. Planta, 2007, 226, 1475-1490.	3.2	70
136	Cell signalling and gene regulation. Current Opinion in Plant Biology, 2003, 6, 405-409.	7.1	69
137	Inheritance of Trans Chromosomal Methylation patterns from <i>Arabidopsis</i> F1 hybrids. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2017-2022.	7.1	69
138	Insertion and Excision of Ds Controlling Elements in Maize. Cold Spring Harbor Symposia on Quantitative Biology, 1984, 49, 347-354.	1.1	69
139	Anaerobically regulated aldolase gene of maize. Journal of Molecular Biology, 1988, 202, 759-767.	4.2	67
140	Expression of pathogenesis-related genes in cotton stems in response to infection by Verticillium dahliae. Physiological and Molecular Plant Pathology, 2001, 58, 119-131.	2.5	67
141	Site specificity of the Arabidopsis METI DNA methyltransferase demonstrated through hypermethylation of the superman locus. Plant Molecular Biology, 2001, 46, 171-183.	3.9	67
142	Ds tagging of BRANCHED FLORETLESS 1 (BFL1) that mediates the transition from spikelet to floret meristem in rice (Oryza sativa L). BMC Plant Biology, 2003, 3, 6.	3.6	67
143	Molecular analysis of the alcohol dehydrogenase gene family of barley. Plant Molecular Biology, 1988, 11, 147-160.	3.9	66
144	Saturation mutagenesis of the octopine synthase enhancer: correlation of mutant phenotypes with binding of a nuclear protein factor.. Proceedings of the National Academy of Sciences of the United States of America, 1989, 86, 3733-3737.	7.1	66

#	Article	IF	Citations
145	UBIQUITIN-SPECIFIC PROTEASE 26 Is Required for Seed Development and the Repression of <i>PHERES1</i> in Arabidopsis. Genetics, 2008, 180, 229-236.	2.9	66
146	An iAc/Ds gene and enhancer trapping system for insertional mutagenesis in rice. Functional Plant Biology, 2002, 29, 547.	2.1	65
147	Histone Acetylation, VERNALIZATION INSENSITIVE 3 , FLOWERING LOCUS C , and the Vernalization Response. Molecular Plant, 2009, 2, 724-737.	8.3	64
148	Enhancing the Anaerobic Response. Annals of Botany, 2003, 91, 111-117.	2.9	63
149	Expression of a bacterial gene in transgenic tobacco plants confers resistance to the herbicide 2,4-dichlorophenoxyacetic acid. Plant Molecular Biology, 1989, 13, 533-540.	3.9	61
150	Isolation and characterization of a Ds-tagged rice (Oryza sativa L.) GA-responsive dwarf mutant defective in an early step of the gibberellin biosynthesis pathway. Plant Cell Reports, 2005, 23, 819-833.	5.6	61
151	Epigenetics in plantsâ€"vernalisation and hybrid vigour. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2011, 1809, 427-437.	1.9	61
152	In Nicotiana species, an artificial microRNA corresponding to the virulence modulating region of Potato spindle tuber viroid directs RNA silencing of a soluble inorganic pyrophosphatase gene and the development of abnormal phenotypes. Virology, 2014, 450-451, 266-277.	2.4	61
153	Autoradiography of the Bacillus subtilis chromosome. Journal of Molecular Biology, 1966, 15, 435-IN3.	4.2	59
154	<i>VERNALIZATION INSENSITIVE 3</i> (<i>VIN3</i>) is required for the response of <i>Arabidopsis thaliana</i> seedlings exposed to low oxygen conditions. Plant Journal, 2009, 59, 576-587.	5.7	59
155	Identification of High-Temperature-Responsive Genes in Cereals Â Â. Plant Physiology, 2012, 158, 1439-1450.	4.8	59
156	Identification of candidate genes for fusarium yellows resistance in Chinese cabbage by differential expression analysis. Plant Molecular Biology, 2014, 85, 247-257.	3.9	57
157	A tissue culture induced Adh1 null mutant of maize results from a single base change. Molecular Genetics and Genomics, 1987, 210, 181-183.	2.4	56
158	A quick and easy method for isolating good-quality RNA from cotton (Gossypium hirsutum L.) tissues. Plant Molecular Biology Reporter, 2002, 20, 213-218.	1.8	56
159	Mechanisms of gene repression by vernalization in Arabidopsis. Plant Journal, 2009, 59, 488-498.	5.7	56
160	Organ regulated expression of the Parasponia andersonii haemoglobin gene in transgenic tobacco plants. Molecular Genetics and Genomics, 1988, 214, 68-73.	2.4	55
161	Simple sequence repeat (SSR) markers reveal low levels of polymorphism between cotton (Gossypium) Tj ETQq1 1 0.784314 rgBT /Ove	1.5	55
162	Title is missing!. Molecular Breeding, 1999, 5, 219-232.	2.1	54

#	Article	IF	Citations
163	Overexpression of alcohol dehydrogenase or pyruvate decarboxylase improves growth of hairy roots at reduced oxygen concentrations. Biotechnology and Bioengineering, 2002, 77, 455-461.	3.3	54
164	Molecular Mechanisms of Epigenetic Variation in Plants. International Journal of Molecular Sciences, 2012, 13, 9900-9922.	4.1	54
165	Cloning and characterization of microRNAs from <i>Brassica napus</i>. FEBS Letters, 2007, 581, 3848-3856.	2.8	52
166	Vernalization in cereals. Journal of Biology, 2009, 8, 57.	2.7	52
167	Dissociation (Ds) constructs, mapped Ds launch pads and a transiently-expressed transposase system suitable for localized insertional mutagenesis in rice. Theoretical and Applied Genetics, 2006, 112, 1326-1341.	3.6	51
168	Hybrid mimics and hybrid vigor in <i>Arabidopsis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4959-67.	7.1	51
169	Cotton plants transformed with a bacterial degradation gene are protected from accidental spray drift damage by the herbicide 2,4-dichlorophenoxyacetic acid. Transgenic Research, 1993, 2, 162-169.	2.4	49
170	Genetic distance of inbred lines of Chinese cabbage and its relationship to heterosis. Plant Gene, 2016, 5, 1-7.	2.3	48
171	Hairpin RNAs derived from RNA polymerase II and polymerase III promoter-directed transgenes are processed differently in plants. Rna, 2008, 14, 903-913.	3.5	47
172	Comparisons of early transcriptome responses to low-oxygen environments in three dicotyledonous plant species. Plant Signaling and Behavior, 2010, 5, 1006-1009.	2.4	47
173	Agrobacterium tumefaciens-gene transfer into wheat tissues. Plant Cell, Tissue and Organ Culture, 1991, 25, 209-218.	2.3	46
174	Isolation of the glucose oxidase gene from Talaromyces flavus and characterisation of its role in the biocontrol of Verticillium dahliae. Current Genetics, 1997, 32, 367-375.	1.7	45
175	Molecular and cellular characteristics of hybrid vigour in a commercial hybrid of Chinese cabbage. BMC Plant Biology, 2016, 16, 45.	3.6	45
176	Cell-Specific Expression of the Promoters of Two Nonlegume Hemoglobin Genes in a Transgenic Legume, Lotus corniculatus. Plant Physiology, 1997, 113, 45-57.	4.8	44
177	The low temperature response pathways for cold acclimation and vernalization are independent. Plant, Cell and Environment, 2011, 34, 1737-1748.	5.7	43
178	Characterization of pyruvate decarboxylase genes from rice. Plant Molecular Biology, 1996, 31, 761-770.	3.9	42
179	Long noncoding RNAs in Brassica rapa L. following vernalization. Scientific Reports, 2019, 9, 9302.	3.3	42
180	The Use of the Emu Promoter With Antibiotic and Herbicide Resistance Genes for the Selection of Transgenic Wheat Callus and Rice Plants. Functional Plant Biology, 1994, 21, 95.	2.1	41

#	Article	IF	Citations
181	Comparison of three selectable marker genes for transformation of wheat by microprojectile bombardment. Functional Plant Biology, 1998, 25, 39.	2.1	41
182	Long non-coding RNA-mediated mechanisms independent of the RNAi pathway in animals and plants. RNA Biology, 2011, 8, 404-414.	3.1	41
183	Cytogenetics of the parthenogenetic grasshopper Warramaba virgo and its bisexual relatives. Chromosoma, 1982, 85, 181-199.	2.2	40
184	Regulation of the Arabidopsis Adh Gene by Anaerobic and Other Environmental Stresses. Annals of Botany, 1994, 74, 301-308.	2.9	40
185	A bidirectional gene trap construct suitable for T-DNA and Ds-mediated insertional mutagenesis in rice (Oryza sativa L.). Plant Biotechnology Journal, 2004, 2, 367-380.	8.3	40
186	Effective ribozyme delivery in plant cells.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 6175-6179.	7.1	39
187	Ovule and embryo development, apomixis and fertilization. Current Opinion in Plant Biology, 1998, 1, 26-31.	7.1	39
188	Molecular analysis of the ADH1-C m allele of maize. Plant Molecular Biology, 1989, 13, 203-212.	3.9	38
189	Hemoglobin genes in non-legumes: cloning and characterization of a Casuarina glauca hemoglobin gene. Plant Molecular Biology, 1991, 16, 339-344.	3.9	38
190	Polycomb proteins regulate the quantitative induction of <i>VERNALIZATION INSENSITIVE 3</i> in response to low temperatures. Plant Journal, 2011, 65, 382-391.	5.7	38
191	Tissue and cell-specific transcriptomes in cotton reveal the subtleties of gene regulation underlying the diversity of plant secondary cell walls. BMC Genomics, 2017, 18, 539.	2.8	38
192	Response of larval Chironomus tepperi (Diptera: Chironomidae) to individual Bacillus thuringiensis var. israelensis toxins and toxin mixtures. Journal of Invertebrate Pathology, 2005, 88, 34-39.	3.2	37
193	Early changes of gene activity in developing seedlings of Arabidopsis hybrids relative to parents may contribute to hybrid vigour. Plant Journal, 2016, 88, 597-607.	5.7	37
194	Twenty-fourâ€“nucleotide siRNAs produce heritable trans-chromosomal methylation in F1 <i>Arabidopsis</i> hybrids. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6895-E6902.	7.1	36
195	TheDsltransposable element acts as an intron in the mutant alleleAdh1-Fm335and is spliced from the message. Nucleic Acids Research, 1988, 16, 3815-3828.	14.5	35
196	Microarray Analysis Reveals Vegetative Molecular Phenotypes of Arabidopsis Flowering-time Mutants. Plant and Cell Physiology, 2005, 46, 1190-1201.	3.1	35
197	PIF4-controlled auxin pathway contributes to hybrid vigor in <i>Arabidopsis thaliana</i>. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3555-E3562.	7.1	35
198	Opposing effects of reduced DNA methylation on flowering time in Arabidopsis thaliana. Planta, 2003, 216, 461-466.	3.2	34

#	Article	IF	Citations
199	Transgene structures suggest that multiple mechanisms are involved in T-DNA integration in plants. Plant Science, 2006, 171, 308-322.	3.6	34
200	Epigenetic variation in the <i>FWA</i> gene within the genus Arabidopsis. Plant Journal, 2011, 66, 831-843.	5.7	34
201	Members of the MYBMIXTA-like transcription factors may orchestrate the initiation of fiber development in cotton seeds. Frontiers in Plant Science, 2014, 5, 179.	3.6	33
202	Satellite RNAs interfere with the function of viral RNA silencing suppressors. Frontiers in Plant Science, 2015, 6, 281.	3.6	33
203	Vernalization and the initiation of flowering. Seminars in Cell and Developmental Biology, 1996, 7, 441-448.	5.0	32
204	<i>DEMETER</i> plays a role in DNA demethylation and disease response in somatic tissues of Arabidopsis. Epigenetics, 2019, 14, 1074-1087.	2.7	32
205	The FLX Gene of Arabidopsis is Required for FRI-Dependent Activation of FLC Expression. Plant and Cell Physiology, 2007, 49, 191-200.	3.1	31
206	Effects of manipulation of pyruvate decarboxylase and alcohol dehydrogenase levels on the submergence tolerance of rice. Functional Plant Biology, 2001, 28, 1231.	2.1	31
207	Behaviour of modified Ac elements in flax callus and regenerated plants. Plant Molecular Biology, 1993, 22, 625-633.	3.9	30
208	Cytokinin synthesis is higher in the Arabidopsis amp1 mutant. Plant Growth Regulation, 2000, 32, 267-273.	3.4	30
209	Genetic contributions to agricultural sustainability. Philosophical Transactions of the Royal Society B: Biological Sciences, 2008, 363, 591-609.	4.0	30
210	Development of primer sets that can verify the enrichment of histone modifications, and their application to examining vernalization-mediated chromatin changes in <i>Brassica rapa</i> L.. Genes and Genetic Systems, 2016, 91, 1-10.	0.7	29
211	The Arabidopsis thaliana genome has multiple divergent forms of phosphoinositol-specific phospholipase C. Gene, 1997, 202, 151-156.	2.2	28
212	Transgene Expression and Transgene-Induced Silencing in Diploid and Autotetraploid Arabidopsis. Genetics, 2011, 187, 409-423.	2.9	28
213	Nicotiana Small RNA Sequences Support a Host Genome Origin of Cucumber Mosaic Virus Satellite RNA. PLoS Genetics, 2015, 11, e1004906.	3.5	28
214	Trichomes control flower bud shape by linking together young petals. Nature Plants, 2016, 2, 16093.	9.3	28
215	The role of FRIGIDA and FLOWERING LOCUS C genes in flowering time of Brassica rapa leafy vegetables. Scientific Reports, 2019, 9, 13843.	3.3	27
216	Leaf growth in early development is key to biomass heterosis in Arabidopsis. Journal of Experimental Botany, 2020, 71, 2439-2450.	4.8	27

#	Article	IF	Citations
217	Factors influencing stable transformation of maize protoplasts by electroporation. Plant Cell, Tissue and Organ Culture, 1989, 18, 281-296.	2.3	26
218	Transcription of the maize transposable element Ac in maize seedlings and in transgenic tobacco. Molecular Genetics and Genomics, 1988, 212, 505-509.	2.4	25
219	The expression and anaerobic induction of alcohol dehydrogenase in cotton. Biochemical Genetics, 1994, 32, 279-300.	1.7	25
220	Vernalization: Spring into Flowering. Developmental Cell, 2006, 11, 1-2.	7.0	25
221	Genome-wide characterization of DNA methylation, small RNA expression, and histone H3 lysine nine di-methylation in <i>Brassica rapa</i> L.. DNA Research, 2018, 25, 511-520.	3.4	25
222	The histone modification H3 lysine 27 tri-methylation has conserved gene regulatory roles in the triplicated genome of Brassica rapa L.. DNA Research, 2019, 26, 433-443.	3.4	25
223	The Ds1 controlling element family in maize andTripsacum. Journal of Molecular Evolution, 1987, 26, 329-334.	1.8	24
224	Investigation of the chromosomal location of the bacterial blight resistance gene present in an Australian cotton (Gossypium hirsutum L.) cultivar. Australian Journal of Agricultural Research, 2002, 53, 551.	1.5	24
225	Genome wide gene expression in artificially synthesized amphidiploids of Arabidopsis. Plant Molecular Biology, 2011, 77, 419-431.	3.9	24
226	Multiple Mechanisms and Challenges for the Application of Allopolyploidy in Plants. International Journal of Molecular Sciences, 2012, 13, 8696-8721.	4.1	24
227	Trans-chromosomal methylation. Epigenetics, 2012, 7, 800-805.	2.7	24
228	A TM3-like MADS-box gene from Eucalyptus expressed in both vegetative and reproductive tissues. Gene, 1999, 228, 155-160.	2.2	23
229	Genome-wide analyses of four major histone modifications in Arabidopsis hybrids at the germinating seed stage. BMC Genomics, 2017, 18, 137.	2.8	23
230	The maize transposable element Ac excises in progeny of transformed tobacco. Plant Molecular Biology, 1989, 13, 109-118.	3.9	22
231	Cotyledons contribute to plant growth and hybrid vigor in Arabidopsis. Planta, 2019, 249, 1107-1118.	3.2	22
232	Symbiotic and Nonsymbiotic Hemoglobin Genes of Casuarina glauca. Plant Cell, 1995, 7, 213.	6.6	21
233	The alcohol dehydrogenase genes of cotton. Plant Molecular Biology, 1996, 31, 897-904.	3.9	21
234	Cycloheximide treatment of cotton ovules alters the abundance of specific classes of mRNAs and generates novel ESTs for microarray expression profiling. Molecular Genetics and Genomics, 2005, 274, 477-493.	2.1	21

#	Article	IF	Citations
235	Senescence and Defense Pathways Contribute to Heterosis. Plant Physiology, 2019, 180, 240-252.	4.8	21
236	Cloning and Sequencing of a Full-Length cDNA from Thlaspi arvense L. That Encodes a Cytochrome P-450. Plant Physiology, 1994, 105, 755-756.	4.8	20
237	Comparison of transcriptome profiles by Fusarium oxysporum inoculation between Fusarium yellows resistant and susceptible lines in Brassica rapa L.. Plant Cell Reports, 2017, 36, 1841-1854.	5.6	20
238	Genome Triplication Leads to Transcriptional Divergence of FLOWERING LOCUS C Genes During Vernalization in the Genus Brassica. Frontiers in Plant Science, 2020, 11, 619417.	3.6	20
239	Post-Translational Modifications of the Endogenous and Transgenic FLC Protein in Arabidopsis thaliana. Plant and Cell Physiology, 2008, 49, 1859-1866.	3.1	19
240	Analysis of Argonaute 4-Associated Long Non-Coding RNA in Arabidopsis thaliana Sheds Novel Insights into Gene Regulation through RNA-Directed DNA Methylation. Genes, 2017, 8, 198.	2.4	19
241	Early Establishment of Photosynthesis and Auxin Biosynthesis Plays a Key Role in Early Biomass Heterosis in Brassica napus (Canola) Hybrids. Plant and Cell Physiology, 2020, 61, 1134-1143.	3.1	19
242	Tobacco Genes Expressed during in vitro Floral Initiation and Their Expression during Normal Plant Development. Plant Cell, 1989, 1, 25.	6.6	18
243	A novel T-DNA vector design for selection of transgenic lines with simple transgene integration and stable transgene expression. Functional Plant Biology, 2005, 32, 671.	2.1	18
244	Genes Directing Flower Development in Arabidopsis. Plant Cell, 2019, 31, 1192-1193.	6.6	18
245	Genetic Control of Male Fertility in Higher Plants. Functional Plant Biology, 1992, 19, 419.	2.1	18
246	Segmental amplification in a satellite DNA: Restriction enzyme analysis of the major satellite ofMacropus rufogriseus. Chromosoma, 1980, 79, 179-198.	2.2	17
247	A primaeval origin for plant and animal haemoglobins?. Australian Systematic Botany, 1990, 3, 81.	0.9	17
248	Cytogenetics of the parthenogenetic grasshopper Warramaba virgo and its bisexual relatives. Chromosoma, 1981, 82, 453-469.	2.2	16
249	Promoter Elements Required for Developmental Expression of the Maize Adh1 Gene in Transgenic Rice. Plant Cell, 1994, 6, 799.	6.6	16
250	Transposable Elements Can Be Used to Study Cell Lineages in Transgenic Plants. Plant Cell, 1989, 1, 757.	6.6	15
251	Nonlegume Hemoglobin Genes Retain Organ-Specific Expression in Heterologous Transgenic Plants. Plant Cell, 1990, 2, 633.	6.6	15
252	Nucleotide Sequence of a Rice Genomic Pyruvate Decarboxylase Gene That Lacks Introns: A Pseudo-Gene?. Plant Physiology, 1994, 106, 1697-1698.	4.8	15

#	Article	IF	Citations
253	Molecular Basis of the Anaerobic Response in Plants. IUBMB Life, 2001, 51, 79-82.	3.4	15
254	A ribozyme gene and an antisense gene are equally effective in conferring resistance to tobacco mosaic virus on transgenic tobacco. Molecular Genetics and Genomics, 1996, 250, 329.	2.4	15
255	Genetic characterization of inbred lines of Chinese cabbage by DNA markers; towards the application of DNA markers to breeding of F1 hybrid cultivars. Data in Brief, 2016, 6, 229-237.	1.0	14
256	Patterns of gene expression in developing embryos of Arabidopsis hybrids. Plant Journal, 2017, 89, 927-939.	5.7	14
257	A prolonged cold treatment-induced cytochrome P450 gene from Arabidopsis thaliana. Plant, Cell and Environment, 1999, 22, 791-800.	5.7	12
258	Thetms2 gene as a negative selection marker in rice. Plant Molecular Biology Reporter, 2000, 18, 227-233.	1.8	12
259	compact shoot and leafy head 1, a mutation affects leaf initiation and developmental transition in rice (Oryza sativa L.). Plant Cell Reports, 2007, 26, 421-427.	5.6	12
260	Effectiveness of Purified Bacillus thuringiensis Berliner Insecticidal Proteins in Controlling Three Insect Pests of Australian Eucalypt Plantations. Journal of Economic Entomology, 1996, 89, 1392-1398.	1.8	11
261	Molecular Basis of the Anaerobic Response in Plants. IUBMB Life, 2001, 51, 79-82.	3.4	11
262	The hunt for hypoxia responsive natural antisense short interfering RNAs. Plant Signaling and Behavior, 2010, 5, 247-251.	2.4	11
263	A comparison of transcriptome and epigenetic status between closely related species in the genus Arabidopsis. Gene, 2012, 506, 301-309.	2.2	11
264	Repeated DNA Sequences and Kangaroo Phylogeny. Australian Journal of Biological Sciences, 1981, 34, 325.	0.5	11
265	Genomic approaches to the discovery of promoters for sustained expression in cotton (Gossypium) Tj ETQq1 1 0.784314 rgBT /Overlo Rubisco small subunit promoter identified using EST sequence analysis and cDNA microarrays. Plant Biotechnology, 2006, 23, 437-450.	1.0	11
266	Manipulating floral organ identity. Current Biology, 1993, 3, 90-93.	3.9	9
267	Searching for tagged male-sterile mutants of arabidopsis. Plant Molecular Biology Reporter, 1996, 14, 330-342.	1.8	9
268	Hypoxia. Plant Signaling and Behavior, 2009, 4, 773-776.	2.4	9
269	Characterization of Histone H3 Lysine 4 and 36 Tri-methylation in Brassica rapa L.. Frontiers in Plant Science, 2021, 12, 659634.	3.6	9
270	Transgenic cotton (Gossypium hirsutum) over-expressing alcohol dehydrogenase shows increased ethanol fermentation but no increase in tolerance to oxygen deficiency. Functional Plant Biology, 2000, 27, 1041.	2.1	8

#	Article	IF	Citations
271	Genome-wide analysis of long noncoding RNAs, 24-nt siRNAs, DNA methylation and H3K27me3 marks in Brassica rapa. PLoS ONE, 2021, 16, e0242530.	2.5	8
272	Transcriptional Association between mRNAs and Their Paired Natural Antisense Transcripts Following Fusarium oxysporum Inoculation in Brassica rapa L.. Horticulturae, 2022, 8, 17.	2.8	8
273	The transcriptional response to salicylic acid plays a role in Fusarium yellows resistance in Brassica rapa L.. Plant Cell Reports, 2021, 40, 605-619.	5.6	7
274	The Molecular Basis of Cold-Induced Pollen Sterility in Rice. , 2007, , 205-207.		7
275	Phenotyping cotton ovule fibre initiation with spatial statistics. Australian Journal of Botany, 2007, 55, 608.	0.6	7
276	Transcription from a plant gene promoter in animal cells. Nucleic Acids Research, 1985, 13, 7945-7957.	14.5	6
277	Protein Synthesis During Oxygen Deprivation in Cotton. Functional Plant Biology, 1996, 23, 341.	2.1	6
278	Isolation of an ent-kaurene oxidase cDNA from Cucurbita maxima. Functional Plant Biology, 2000, 27, 1141.	2.1	6
279	Sequencing and Utilization of the Gossypium Genomes. Tropical Plant Biology, 2010, 3, 71-74.	1.9	6
280	In Arabidopsis hybrids and Hybrid Mimics, upâ€regulation of cell wall biogenesis is associated with the increased plant size. Plant Direct, 2019, 3, e00174.	1.9	6
281	Isolation and characterisation of full-length cDNA clones of the giant taro (Alocasia macrorrhiza) trypsin/chymotrypsin inhibitor. Plant Molecular Biology, 1996, 30, 1035-1039.	3.9	5
282	SPT5â€like, a new component in plant RdDM. EMBO Reports, 2009, 10, 573-575.	4.5	5
283	Arabidopsis Col/Ler and Ws/Ler hybrids and Hybrid Mimics produce seed yield heterosis through increased height, inflorescence branch and silique number. Planta, 2020, 252, 40.	3.2	5
284	Development of a New DNA Marker for Fusarium Yellows Resistance in Brassica rapa Vegetables. Plants, 2021, 10, 1082.	3.5	5
285	Construction of a YAC Contig of 2 Megabases Around the MS1 Gene in Arabidopsis thaliana. Functional Plant Biology, 1996, 23, 453.	2.1	5
286	Rice Gene Machine: A Vehicle for Finding Functions of Cereal Genes. Asia Pacific Biotech News, 2002, 06, 936-942.	0.0	4
287	Isolation and functional characterization of cytochrome P450s in Gibberellin biosynthesis pathway. Methods in Enzymology, 2002, 357, 381-388.	1.0	4
288	Integration of seasonal flowering time responses in temperate cereals. Plant Signaling and Behavior, 2008, 3, 601-602.	2.4	4

#	Article	IF	Citations
289	Maize Alcohol Dehydrogenase: A Molecular Perspective. Plant Gene Research, 1986, , 73-100.	0.4	4
290	Electron Microscopic Evidence for a Multimeric System of Plasmids in Fast-Growing Rhizobium Spp.. Australian Journal of Biological Sciences, 1979, 32, 651.	0.5	4
291	Trichomes at the Base of the Petal Are Regulated by the Same Transcription Factors as Cotton Seed Fibers. Plant and Cell Physiology, 2020, 61, 1590-1599.	3.1	3
292	Rice hybrid mimics have stable yields equivalent to those of the F1 hybrid and suggest a basis for hybrid vigour. Planta, 2021, 254, 51.	3.2	3
293	Synthesis of complementary RNA by RNA-dependent RNA polymerases in plant extracts is independent of an RNA primer. Functional Plant Biology, 2008, 35, 1091.	2.1	3
294	Forefronts of Flowering. Plant Cell, 1992, 4, 867-870.	6.6	3
295	Title is missing!. Australasian Plant Pathology, 2001, 30, 27.	1.0	2
296	The Arabidopsis AMP1 Gene Encodes a Putative Glutamate Carboxypeptidase. Plant Cell, 2001, 13, 2115.	6.6	2
297	Approaches for the Isolation ofArabidopsisadh1Regulatory Mutants Using Allyl Alcohol Selection. Russian Journal of Plant Physiology, 2003, 50, 762-773.	1.1	2
298	Polycomb repression. Plant Signaling and Behavior, 2008, 3, 412-414.	2.4	2
299	In Arabidopsis thaliana Heterosis Level Varies among Individuals in an F1 Hybrid Population. Plants, 2020, 9, 414.	3.5	2
300	Capturing hybrid vigor for lentil breeding. Crop Science, 2022, 62, 1787-1796.	1.8	2
301	Modification of Vacuolar Chitinase and Osmotin cDNAs of Tobacco for Extracellular Secretion and their Cloning with CaMV 35S Promoter. Journal of Plant Biochemistry and Biotechnology, 1995, 4, 41-42.	1.7	1
302	Hybrid Vigour and Hybrid Mimics in Japonica Rice. Agronomy, 2022, 12, 1559.	3.0	1
303	Aspects of the ac/ds transposable element system in maize. Journal of Cell Science, 1987, 1987, 123-138.	2.0	0
304	A DNA-Binding Protein Factor Recognizes Two Binding Domains within the Octopine Synthase Enhancer Element. Plant Cell, 1990, 2, 215.	6.6	0
305	Rice Genomics. , 2010, , 257-279.		0
306	Gene-Expression Following T-DNA Transfer Into Plant Cells Is Aphidicolin-Sensitive. Functional Plant Biology, 1994, 21, 125.	2.1	0